

#9

1646

TECH CENTER 1600/2900

JAN 10 2002

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DATE: 12/28/2001  
TIME: 16:10:51RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,458Input Set : A:\13198.asc  
Output Set: N:\CRF3\12282001\I424458.raw

P.S.

4 <110> APPLICANT: Hayward, Nicholas  
 5 Silins, Ginters  
 6 Grimmond, Sean  
 7 Gartside, Michael  
 8 Hancock, John  
 10 <120> TITLE OF INVENTION: A NOVEL GENE AND USES THEREFOR  
 12 <130> FILE REFERENCE: 13198  
 14 <140> CURRENT APPLICATION NUMBER: 09/424,458  
 15 <141> CURRENT FILING DATE: 2000-03-16  
 17 <150> PRIOR APPLICATION NUMBER: PCT/AU98/00380  
 18 <151> PRIOR FILING DATE: 1998-05-22  
 20 <160> NUMBER OF SEQ ID NOS: 111  
 22 <170> SOFTWARE: PatentIn Ver. 2.1  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 8  
 26 <212> TYPE: PRT  
 27 <213> ORGANISM: Artificial Sequence  
 29 <220> FEATURE:  
 30 <223> OTHER INFORMATION: Description of Artificial Sequence:Peptide repeat motif in DnaJ homologues.  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: UNSURE  
 35 <222> LOCATION: (2)..(3)  
 36 <223> OTHER INFORMATION: Xaa at position 2,3 can be any amino acid.  
 38 <220> FEATURE:  
 39 <221> NAME/KEY: UNSURE  
 40 <222> LOCATION: (5)  
 41 <223> OTHER INFORMATION: Xaa at position 5 can be any amino acid.  
 43 <220> FEATURE:  
 44 <221> NAME/KEY: UNSURE  
 45 <222> LOCATION: (7)  
 46 <223> OTHER INFORMATION: Xaa at position 7 can be any amio acid.  
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 49 Cys Xaa Xaa Cys Xaa Gly Xaa Gly  
 50 1 5  
 53 <210> SEQ ID NO: 2  
 54 <211> LENGTH: 1242  
 55 <212> TYPE: DNA  
 56 <213> ORGANISM: Homo sapiens  
 58 <220> FEATURE:  
 59 <221> NAME/KEY: CDS  
 60 <222> LOCATION: (30)..(959)  
 62 <400> SEQUENCE: 2  
 63 tcagtaaaca cagagactgg ggatcgatc atg ggg ctt tgt aag tgc ccc aag 53  
 65 Met Gly Leu Cys Lys Cys Pro Lys  
 66 1 5  
 68 aga aag gtg acc aac ctg ttc tgc ttc gaa cat cgg gtc aac gtc tgc 101

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70	Arg	Lys	Val	Thr	Asn	Leu	Phe	Cys	Phe	Glu	His	Arg	Val	Asn	Val	Cys	
71	10					15						20					
73	gag	cac	tgc	ctg	gta	gcc	aat	cac	gcc	aag	tgc	atc	gtc	cag	tcc	tac	149
75	Glu	His	Cys	Leu	Val	Ala	Asn	His	Ala	Lys	Cys	Ile	Val	Gln	Ser	Tyr	
76	25					30						35					40
78	ctg	caa	tgg	ctc	caa	gat	agc	gac	tac	aac	ccc	aat	tgc	cgc	ctg	tgc	197
80	Leu	Gln	Trp	Leu	Gln	Asp	Ser	Asp	Tyr	Asn	Pro	Asn	Cys	Arg	Leu	Cys	
81						45					50						55
83	aac	ata	ccc	ctg	gcc	agg	cga	gag	acg	acc	cgc	ctt	gtc	tgc	tat	gat	245
85	Asn	Ile	Pro	Leu	Ala	Ser	Arg	Glu	Thr	Thr	Arg	Leu	Val	Cys	Tyr	Asp	
86						60					65						70
88	ctc	ttt	cac	tgg	gcc	tgc	ctc	aat	gaa	cgt	gct	gcc	cag	cta	ccc	cga	293
90	Leu	Phe	His	Trp	Ala	Cys	Leu	Asn	Glu	Arg	Ala	Ala	Gln	Leu	Pro	Arg	
91						75					80						85
93	aac	acg	gca	cct	gcc	ggc	tat	cag	tgc	ccc	agc	tgc	aat	ggc	ccc	atc	341
95	Asn	Thr	Ala	Pro	Ala	Gly	Tyr	Gln	Cys	Pro	Ser	Cys	Asn	Gly	Pro	Ile	
96						90					95						100
98	ttc	ccc	cca	acc	aac	ctg	gct	ggc	ccc	gtg	gcc	tcc	gca	ctg	aga	gag	389
100	Phe	Pro	Pro	Thr	Asn	Leu	Ala	Gly	Pro	Val	Ala	Ser	Ala	Leu	Arg	Glu	
101	105					105					110			115			120
103	aag	ctg	gcc	aca	gtc	aac	tgg	gcc	cgg	gca	gga	ctg	ggc	ctc	cct	ctg	437
105	Lys	Leu	Ala	Thr	Val	Asn	Trp	Ala	Arg	Ala	Gly	Leu	Gly	Leu	Pro	Leu	
106						125					130			135			
108	atc	gat	gag	gtg	gtg	agc	cca	gag	ccc	gag	ccc	ctc	aac	acg	tct	gac	485
110	Ile	Asp	Glu	Val	Val	Ser	Pro	Glu	Pro	Glu	Pro	Leu	Asn	Thr	Ser	Asp	
111						140					145			150			
113	ttc	tct	gac	tgg	tct	agt	ttt	aat	gcc	agc	agt	acc	cct	gga	cca	gag	533
116	Phe	Ser	Asp	Trp	Ser	Ser	Phe	Asn	Ala	Ser	Ser	Thr	Pro	Gly	Pro	Glu	
117						155					160			165			
119	gag	gta	gac	agc	gcc	tct	gct	gcc	cca	gcc	ttc	tac	agc	cga	gcc	ccc	581
121	Glu	Val	Asp	Ser	Ala	Ser	Ala	Ala	Pro	Ala	Phe	Tyr	Ser	Arg	Ala	Pro	
122						170					175			180			
124	cgg	ccc	cca	gct	tcc	cca	ggc	cgg	ccc	gag	cag	cac	aca	gtg	atc	cac	629
126	Arg	Pro	Pro	Ala	Ser	Pro	Gly	Arg	Pro	Glu	Gln	His	Thr	Val	Ile	His	
127	185					185					190			195			200
129	atg	ggc	aat	cct	gag	ccc	ttg	act	cac	gcc	cct	agg	aag	gtg	tat	gat	677
131	Met	Gly	Asn	Pro	Glu	Pro	Leu	Thr	His	Ala	Pro	Arg	Lys	Val	Tyr	Asp	
132						205					210			215			
134	acg	cgg	gat	gat	gac	cgg	aca	cca	ggc	ctc	cat	gga	gac	tgt	gac	gat	725
136	Thr	Arg	Asp	Asp	Asp	Arg	Thr	Pro	Gly	Leu	His	Gly	Asp	Cys	Asp	Asp	
137						220					225			230			
139	gac	aag	tac	cga	cgt	cg	ccg	gcc	ttg	ggt	tgg	ctg	gcc	cg	ctg	cta	773
141	Asp	Lys	Tyr	Arg	Arg	Arg	Pro	Ala	Leu	Gly	Trp	Leu	Ala	Arg	Leu	Leu	
142						235					240			245			
144	agg	agc	cgg	gct	ggg	tct	cg	aag	cgg	ccg	ctg	acc	ctg	ctc	cag	cgg	821
146	Arg	Ser	Arg	Ala	Gly	Ser	Arg	Lys	Arg	Pro	Leu	Thr	Leu	Leu	Gln	Arg	
147						250					255			260			
149	gcg	ggg	ctg	ctg	cta	ctc	ttg	gga	ctg	ctg	ggc	ttc	ctg	gcc	ctc	ttt	869
151	Ala	Gly	Leu	Leu	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Leu	Ala	Leu	Leu	

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152	265	270	275	280
154	gcc ctc atg tct cgc cta ggc cgg gcc gca gct gac agc gat ccc aac			917
156	Ala Leu Met Ser Arg Leu Gly Arg Ala Ala Asp Ser Asp Pro Asn			
157	285	290	295	
159	ctg gac cca ctc atg aac cct cac atc cgc gtg ggc ccc tcc			959
161	Leu Asp Pro Leu Met Asn Pro His Ile Arg Val Gly Pro Ser			
162	300	305	310	
164	ttagccccct tgcttgtggc taggcccagcc taggatgtgg gttctgtgg ggagagggcg 1019			
167	ggtaatgggg aggctgaggg cacctttca ctggccctct ccctcaagcc taagacacta 1079			
170	agaccccaaga cccaaagcca agtccaccag agtggctcg 1139			
173	gtgggtcaag catttgtctt gacttgctt ctcccggtc tccagcctcc gaccctcgc 1199			
176	cccatgaagg agctggcagg tggaaataaa caacaactt att			1242
180	<210> SEQ ID NO: 3			
181	<211> LENGTH: 310			
182	<212> TYPE: PRT			
183	<213> ORGANISM: Homo sapiens			
185	<400> SEQUENCE: 3			
186	Met Gly Leu Cys Lys Cys Pro Lys Arg Lys Val Thr Asn Leu Phe Cys			
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189	Phe Glu His Arg Val Asn Val Cys Glu His Cys Leu Val Ala Asn His			
190	20	25	30	
192	Ala Lys Cys Ile Val Gln Ser Tyr Leu Gln Trp Leu Gln Asp Ser Asp			
193	35	40	45	
195	Tyr Asn Pro Asn Cys Arg Leu Cys Asn Ile Pro Leu Ala Ser Arg Glu			
196	50	55	60	
198	Thr Thr Arg Leu Val Cys Tyr Asp Leu Phe His Trp Ala Cys Leu Asn			
199	65	70	75	80
201	Glu Arg Ala Ala Gln Leu Pro Arg Asn Thr Ala Pro Ala Gly Tyr Gln			
202	85	90	95	
204	Cys Pro Ser Cys Asn Gly Pro Ile Phe Pro Pro Thr Asn Leu Ala Gly			
205	100	105	110	
207	Pro Val Ala Ser Ala Leu Arg Glu Lys Leu Ala Thr Val Asn Trp Ala			
208	115	120	125	
210	Arg Ala Gly Leu Gly Leu Pro Leu Ile Asp Glu Val Val Ser Pro Glu			
211	130	135	140	
213	Pro Glu Pro Leu Asn Thr Ser Asp Phe Ser Asp Trp Ser Ser Phe Asn			
214	145	150	155	160
216	Ala Ser Ser Thr Pro Gly Pro Glu Glu Val Asp Ser Ala Ser Ala Ala			
217	165	170	175	
219	Pro Ala Phe Tyr Ser Arg Ala Pro Arg Pro Pro Ala Ser Pro Gly Arg			
220	180	185	190	
222	Pro Glu Gln His Thr Val Ile His Met Gly Asn Pro Glu Pro Leu Thr			
223	195	200	205	
226	His Ala Pro Arg Lys Val Tyr Asp Thr Arg Asp Asp Asp Arg Thr Pro			
227	210	215	220	
230	Gly Leu His Gly Asp Cys Asp Asp Asp Lys Tyr Arg Arg Arg Pro Ala			
231	225	230	235	240
233	Leu Gly Trp Leu Ala Arg Leu Leu Arg Ser Arg Ala Gly Ser Arg Lys			
234	245	250	255	

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236 Arg Pro Leu Thr Leu Leu Gln Arg Ala Gly Leu Leu Leu Leu Gly  
237 260 265 270  
239 Leu Leu Gly Phe Leu Ala Leu Leu Ala Leu Met Ser Arg Leu Gly Arg  
240 275 280 285  
242 Ala Ala Ala Asp Ser Asp Pro Asn Leu Asp Pro Leu Met Asn Pro His  
243 290 295 300  
245 Ile Arg Val Gly Pro Ser  
246 305 310  
251 <210> SEQ ID NO: 4  
252 <211> LENGTH: 2415  
253 <212> TYPE: DNA  
254 <213> ORGANISM: Homo sapiens  
256 <220> FEATURE:  
257 <221> NAME/KEY: CDS  
258 <222> LOCATION: (3)..(2186)  
260 <400> SEQUENCE: 4  
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263 Ile Ser Phe Leu Ala Pro His Arg Ser Leu Ser Pro Lys Tyr Ser  
264 1 5 10 15  
266 cat ctt gtc cta gcc cat ccc cca gac tat ctc aag gac cag ctg tcc 95  
268 His Leu Val Leu Ala His Pro Pro Asp Tyr Leu Lys Asp Gln Leu Ser  
269 20 25 30  
271 cca cgc ccc cga cct cca cta ggc ctg tgc cac ccg ctg cct gca gga 143  
273 Pro Arg Pro Arg Pro Pro Leu Gly Leu Cys His Pro Leu Pro Ala Gly  
274 35 40 45  
276 aga cgc ccc gtc ccc ggc cgg gtt agc ccc atg gga acg cag cgc ctg 191  
278 Arg Arg Pro Val Pro Gly Arg Val Ser Pro Met Gly Thr Gln Arg Leu  
279 50 55 60  
281 tgt ggc cgc ggg act caa ggc tgg cct ggc tca agt gaa cag cac gtc 239  
283 Cys Gly Arg Gly Thr Gln Gly Trp Pro Gly Ser Ser Glu Gln His Val  
284 65 70 75  
286 cag gag gcg acc tcg tcc gcg ggt ttg cat tct ggg gtg gac gag ctg 287  
288 Gln Glu Ala Thr Ser Ser Ala Gly Leu His Ser Gly Val Asp Glu Leu  
289 80 85 90 95  
291 ggg gtt cgg tcc gag ccc ggt ggg agg ctc ccg gag cgc agc ctg ggc 335  
293 Gly Val Arg Ser Glu Pro Gly Gly Arg Leu Pro Glu Arg Ser Leu Gly  
294 100 105 110  
296 cca gcc cac ccc gcg ccg ggc atg gca ggc acc ctg gac ctg gac 383  
298 Pro Ala His Pro Ala Pro Ala Met Ala Gly Thr Leu Asp Leu Asp  
299 115 120 125  
301 aag ggc tgc acg gtg gag gag ctg ctc ccg ggg tgc atc gaa gcc ttc 431  
303 Lys Gly Cys Thr Val Glu Glu Leu Leu Arg Gly Cys Ile Glu Ala Phe  
304 130 135 140  
306 gat gac tcc ggg aag gtg cgg gac ccg cag ctg gtg cgc atg ttc ctc 479  
308 Asp Asp Ser Gly Lys Val Arg Asp Pro Gln Leu Val Arg Met Phe Leu  
309 145 150 155  
311 atg atg cac ccc tgg tac atc ccc tcc tct cag ctg gcg gcc aag ctg 527  
313 Met Met His Pro Trp Tyr Ile Pro Ser Ser Gln Leu Ala Ala Lys Leu  
314 160 165 170 175

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Output Set: N:\CRF3\12282001\I424458.raw

316	ctc cac atc tac caa caa tcc cgg aag gac aac tcc aat tcc ctg cag	575
318	Leu His Ile Tyr Gln Gln Ser Arg Lys Asp Asn Ser Asn Ser Leu Gln	
319	180 185 190	
321	gtg aaa acg tgc cac ctg gtc agg tac tgg atc tcc gcc ttc cca gcg	623
323	Val Lys Thr Cys His Leu Val Arg Tyr Trp Ile Ser Ala Phe Pro Ala	
324	195 200 205	
326	gag ttt gac ttg aac ccg gag ttg gct gag cag atc aag gag ctg aag	671
328	Glu Phe Asp Leu Asn Pro Glu Leu Ala Glu Gln Ile Lys Glu Leu Lys	
329	210 215 220	
331	gct ctg cta gac caa gaa ggg aac cga cgg cac agc agc cta atc gac	719
333	Ala Leu Leu Asp Gln Glu Gly Asn Arg Arg His Ser Ser Leu Ile Asp	
334	225 230 235	
336	ata gac agc gtc cct acc tac aag tgg aag cgg cag gtg act cag cgg	767
338	Ile Asp Ser Val Pro Thr Tyr Lys Trp Lys Arg Gln Val Thr Gln Arg	
339	240 245 250 255	
341	aac cct gtg gga cag aaa aag cgc aag atg tcc ctg ttg ttt gac cac	815
343	Asn Pro Val Gly Gln Lys Lys Arg Lys Met Ser Leu Leu Phe Asp His	
344	260 265 270	
346	ctg gag ccc atg gag ctg gcg gag cat ctc acc tac ttg gag tat cgc	863
348	Leu Glu Pro Met Glu Leu Ala Glu His Leu Thr Tyr Leu Glu Tyr Arg	
349	275 280 285	
351	tcc ttc tgc aag atc ctg ttt cag gac tat cac agt ttc gtg act cat	911
353	Ser Phe Cys Lys Ile Leu Phe Gln Asp Tyr His Ser Phe Val Thr His	
354	290 295 300	
356	ggc tgc act gtg gac aac ccc gtc ctg gag cgg ttc atc tcc ctc ttc	959
358	Gly Cys Thr Val Asp Asn Pro Val Leu Glu Arg Phe Ile Ser Leu Phe	
359	305 310 315	
361	aac agc gtc tca cag tgg gtg cag ctc atg atc ctc agc aaa ccc aca	1007
363	Asn Ser Val Ser Gln Trp Val Gln Leu Met Ile Leu Ser Lys Pro Thr	
364	320 325 330 335	
366	gcc ccg cag cgg gcc ctg gtc atc aca cac ttt gtc cac gtg gcg gag	1055
368	Ala Pro Gln Arg Ala Leu Val Ile Thr His Phe Val His Val Ala Glu	
369	340 345 350	
371	aag ctg cta cag ctg cag aac ttc aac acg ctg atg gca gtg gtc ggg	1103
373	Lys Leu Leu Gln Leu Gln Asn Phe Asn Thr Leu Met Ala Val Val Gly	
374	355 360 365	
376	ggc ctg agc cac agc tcc atc tcc cgc ctc aag gag acc cac agc cac	1151
378	Gly Leu Ser His Ser Ser Ile Ser Arg Leu Lys Glu Thr His Ser His	
379	370 375 380	
381	gtt agc cct gag acc atc aag ctc tgg gag ggt ctc acg gaa cta gtg	1199
383	Val Ser Pro Glu Thr Ile Lys Leu Trp Glu Gly Leu Thr Glu Leu Val	
384	385 390 395	
386	acg gcg aca ggc aac tat ggc aac tac cgg cgt cgg ctg gca gcc tgt	1247
388	Thr Ala Thr Gly Asn Tyr Gly Asn Tyr Arg Arg Arg Leu Ala Ala Cys	
389	400 405 410 415	
391	gtg ggc ttc cgc ttc ccg atc ctg ggt gtg cac ctc aag gac ctg gtg	1295
393	Val Gly Phe Arg Phe Pro Ile Leu Gly Val His Leu Lys Asp Leu Val	
394	420 425 430	
396	gcc ctg cag ctg gca ctg cct gac tgg ctg gac cca gcc cgg acc cgg	1343

→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY  
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Input Set : A:\13198.asc  
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L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1  
L:1758 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:1761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:1767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:1770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:1773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49  
L:2163 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2166 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2175 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
L:2215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
L:2254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76  
L:2257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76